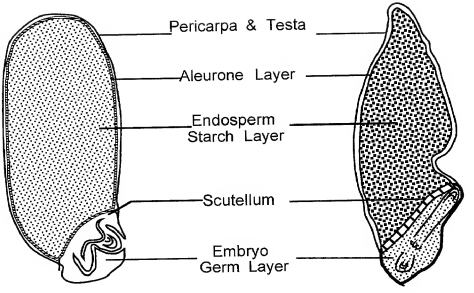
Pericarpa & Testa
Aleurone Layer
Endosperm
Starch Layer
Scutellum
Embryo
Germ Layer

Fig. 1A

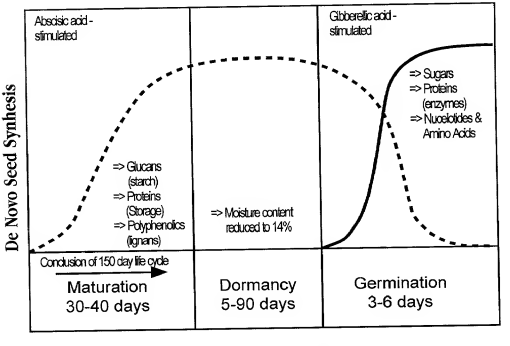
De Novo Seed Synthesis
Abscisic acid - stimulated
=> Glucans (starch)
=> Proteins (Storage)
=> Polyphenolics (lignans)
=> Moisture content reduced to 14%
Gibberellic acid - stimulated
=> Sugars
=> Proteins (enzymes)
=> Nucelotides & Amino Acids
Conclusion of 150 day life cycle
Maturation 30-40 days
Dormancy 5-90 days
Germination 3-6 days

Fig. 1B

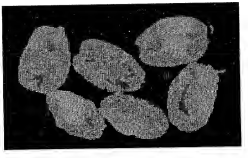

Fig. 1C

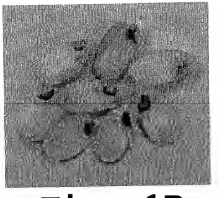

Fig. 1D

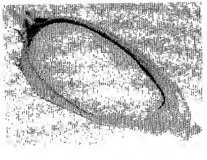

Fig. 1E

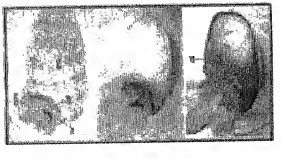

Fig. 1F

```
       10         20         30         40         50         60         70
GGTACCCATC TAATACATTA ATAACAAGAG AGAGAATGGA TAATGCAATT ATTTATTTTT ATGGGAGGCT
CCATGGGTAG ATTATGTAAT TATTGTTCTC TCTCTTACCT ATTACGTTAA TAAATAAAAA TACCCTCCGA

       80         90        100        110        120        130        140
ATATTTTTAT CGGATTTTAG TAAATAACGG GGCAATTCGG TACTTAGGTA AAGCTACGTA TGACTATCGC
TATAAAAATA GCCTAAAATC ATTTATTGCC CCGTTAAGCC ATGAATCCAT TTCGATGCAT ACTGATAGCG

      150        160        170        180        190        200        210
TACCGCTACG GTAGTTGAAT TGGAATTCTT CGATAGCATC TGTTGTGTTG TTGCAGTTAG GGTACTTGAA
ATGGCGATGC CATCAACTTA ACCTTAAGAA GCTATCGTAG ACAACACAAC AACGTCAATC CCATGAACTT

      220        230        240        250        260        270        280
TAGCTCCAGC CGTGAAAACG AGGGGTTTTC GCAGGTTTTA TAGGATTGCC AAGTTAGACT AGGGCAATTC
ATCGAGGTCG GCACTTTTGC TCCCCAAAAG CGTCCAAAAT ATCCTAACGG TTCAATCTGA TCCCGTTAAG

      290        300        310        320        330        340        350
ATGTTCACGG TATTGTGTAG TATATGAAAA AGGAGATCTC CCAAACAATT TATAATTTTG TATAAGGGAG
TACAAGTGCC ATAACACATC ATATACTTTT TCCTCTAGAG GGTTTGTTAA ATATTAAAAC ATATTCCCTC

                                                >AT-rich_region_
                                                |
      360        370        380        390        400        410        420
AAATCGAACT TGAGGTGTCT AATTCACCAA CCGAGCTACT CCCTCCGTTT CATATATGTA TATACATATA
TTTAGCTTGA ACTCCACAGA TTAAGTGGTT GGCTCGATGA GGGAGGCAAA GTATATACAT ATATGTATAT

      430        440        450        460        470        480        490
TACGTATATA TACGTATATA CACATATACG TATATACATA TATGGTATAT ACATATATAT ATATATATAT
ATGCATATAT ATGCATATAT GTGTATATGC ATATATGTAT ATACCATATA TGTATATATA TATATATATA

      500        510        520        530        540        550        560
ATATATATAT ATGTGTGTGT GTGTATGTGG GGTGGCAATG CTAAAAAGTT TTATAATATG AACGGATGAA
TATATATATA TACACACACA CACATACACC CCACCGTTAC GATTTTTCAA AATATTATAC TTGCCTACTT

      570        580        590        600        610        620        630
GTACTATCCA CTAAGTCCCT ATAGTTTTCT GGCACTGTGT AGTATACGAA TGCACAATTA TATCCATAAA
CATGATAGGT GATTCAGGGA TATCAAAAGA CCGTGACACA TCATATGCTT ACGTGTTAAT ATAGGTATTT

      640        650        660        670        680        690        700
ATTGATATTA TATATTCGTC GCGACGAAAA TAAAGACATA ATATTCGGTA TACCATTTAT CCACGATATA
TAACTATAAT ATATAAGCAG CGCTGCTTTT ATTTCTGTAT TATAAGCCAT ATGGTAAATA GGTGCTATAT

      710        720        730        740        750        760        770
TCTAAATTCC ACTGATATAT CTAAATTCCA CTTGATCCCT TTTATGGATA AATTCTGGAT AACAATTACT
AGATTTAAGG TGACTATATA GATTTAAGGT GAACTAGGGA AAATACCTAT TTAAGACCTA TTGTTAATGA

      780        790        800        810        820        830        840
ACCAGCAGTA TATCCTACTA TCAGCGCACT GCACACCAAA CTACCCTCAC CCAGTAGTTA CAAACGCATA
TGGTCGTCAT ATAGGATGAT AGTCGCGTGA CGTGTGGTTT GATGGGAGTG GGTCATCAAT GTTTGCGTAT
```

Fig. 2A

```
       850         860         870         880         890         900         910
TTTTGCCGTT AGTTAATTAT TATCCGGTAA AGAAGGTAAA GAAGATTGGT AGTAATCCAA AATTTTCCCA
AAAACGGCAA TCAATTAATA ATAGGCCATT TCTTCCATTT CTTCTAACCA TCATTAGGTT TTAAAAGGGT

       920         930         940         950         960         970         980
ACCCCAACCT CGGAACAAAA ACCGCGTAGT ATTTGTCGTA ACCAGGAGCA TCCGAGTCAT TAATTTACAC
TGGGGTTGGA GCCTTGTTTT TGGCGCATCA TAAACAGCAT TGGTCCTCGT AGGCTCAGTA ATTAAATGTG

                  >Transcription_start_site
>CAAG_site
                           |                                                 |
       990        1000        1010        1020        1030        1040        1050
CCAAACACAA AAAATTAGCA GCACGCAGCC GCCTTCCCAA TCCTCTCCTC TCTCCTCTCC TCTTCTCCAA
GGTTTGTGTT TTTTAATCGT CGTGCGTCGG CGGAAGGGTT AGGAGAGGAG AGAGGAGAGG AGAAGAGGTT

      1060        1070        1080        1090        1100        1110        1120
GCGGCAATTC GCGCGAGGTT TTCTCCGATC AAACCCTCGA ATCCCCCCCT CGCGAATCCA TCGGAGGGTA
CGCCGTTAAG CGCGCTCCAA AAGAGGCTAG TTTGGGAGCT TAGGGGGGGA GCGCTTAGGT AGCCTCCCAT

      1130        1140        1150        1160        1170        1180
GCCCCGCGAT CCGCGTCGGC GAGAGCGGAT TCCGATTCCG CG ATG GAG CGG GTG TTC TCC GTG
CGGGGCGCTA GGCGCAGCCG CTCTCGCCTA AGGCTAAGGC GC TAC CTC GCC CAC AAG AGG CAC
                                                  M   E   R   V   F   S   V>
                                                 ___a___a__EXON1____a___a___>

     1190        1200        1210        1220        1230        1240
GAG GAG ATC TCC GAC CCA TTC TGG GTC CCG CCT CCG CCG CCG CAG TCG GCG GCG GCG
CTC CTC TAG AGG CTG GGT AAG ACC CAG GGC GGA GGC GGC GGC GTC AGC CGC CGC CGC
 E   E   I   S   D   P   F   W   V   P   P   P   P   P   Q   S   A   A   A>
___a___a___a___a___a___a___a___a__EXON1____a___a___a___a___a___a___a___a___>

       1250        1260        1270        1280        1290
GCC CAG CAG CAG GGC GGC GGC GGC GTG GCT TCG GGA GGT GGT GGT GGT GTA GCG GGG
CGG GTC GTC GTC CCG CCG CCG CCG CAC CGA AGC CCT CCA CCA CCA CCA CAT CGC CCC
 A   Q   Q   Q   G   G   G   G   V   A   S   G   G   G   G   G   V   A   G>
___a___a___a___a___a___a___a___a___a__EXON1____a___a___a___a___a___a___a___>

1300        1310        1320        1330        1340        1350
GGC GGC GGC GGC GGG AAC GCG ATG AAC CGG TGC CCG TCG GAG TGG TAC TTC CAG AAG
CCG CCG CCG CCG CCC TTG CGC TAC TTG GCC ACG GGC AGC CTC ACC ATG AAG GTC TTC
 G   G   G   G   G   N   A   M   N   R   C   P   S   E   W   Y   F   Q   K>
___a___a___a___a___a___a___a___a___a__EXON1____a___a___a___a___a___a___a___>

     1360        1370        1380        1390        1400        1410
TTT CTG GAG GAG GCG GTG CTC GAT AGC CCC GTC CCG AAC CCT AGC CCG AGG GCC GAA
AAA GAC CTC CTC CGC CAC GAG CTA TCG GGG CAG GGC TTG GGA TCG GGC TCC CGG CTT
 F   L   E   E   A   V   L   D   S   P   V   P   N   P   S   P   R   A   E>
___a___a___a___a___a___a___a___a___a__EXON1____a___a___a___a___a___a___a___>
```

Fig. 2B

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        1420          1430          1440          1450          1460
GCG GGA GGG ATC AGG GGC GCA GGA GGG GTG GTG CCG GTC GAT GTT AAG CAG CCG CAG
CGC CCT CCC TAG TCC CCG CGT CCT CCC CAC CAC GGC CAG CTA CAA TTC GTC GGC GTC
 A   G   G   I   R   G   A   G   G   V   V   P   V   D   V   K   Q   P   Q>
___a___a___a___a___a___a___a___a__EXON1____a___a___a___a___a___a___a___a___>

        1470          1480          1490          1500          1510
1520
CTC TCG GCG GCG GCG ACG ACG AGC GCG GTG GTG GAC CCC GTG GAG TAC AAC GCG ATG
GAG AGC CGC CGC CGC TGC TGC TCG CGC CAC CAC CTG GGG CAC CTC ATG TTG CGC TAC
 L   S   A   A   A   T   T   S   A   V   V   D   P   V   E   Y   N   A   M>
___a___a___a___a___a___a___a___a__EXON1____a___a___a___a___a___a___a___a___>

  1530          1540          1550          1560          1570          1580
CTG AAG CAG AAG CTG GAG AAG GAC CTC GCC GCG GTC GCC ATG TGG AGG GTACAGC
GAC TTC GTC TTC GAC CTC TTC CTG GAG CGG CGC CAG CGG TAC ACC TCC CATGTCG
 L   K   Q   K   L   E   K   D   L   A   A   V   A   M   W   R>
___a___a___a___a___a___a____EXON1__a___a___a___a___a___a___a___>

       1590          1600          1610          1620          1630          1640          1650
CATTCTCCCC CCCTCTAGTA CTCGAGAGCT TACTGAGATC GGCAATGCTA GCTACTGTTT GCATCGAATG
GTAAGAGGGG GGGAGATCAT GAGCTCTCGA ATGACTCTAG CCGTTACGAT CGATGACAAA CGTAGCTTAC

       1660          1670          1680          1690          1700          1710          1720
TTTATAGGTA TTTAGATCGG GCATTTCTAT AGACCAATGG CGTCCATGGT CTTGCAATGC GCTCTGTTGA
AAATATCCAT AAATCTAGCC CGTAAAGATA TCTGGTTACC GCAGGTACCA GAACGTTACG CGAGACAACT

       1730          1740          1750          1760          1770          1780          1790
GTGTCGGTGG TTGGTTCGAC TCATAGTATG TAGGGTTGTG CGTATGTACA AACGGAAGCT TCATAGACCT
CACAGCCACC AACCAAGCTG AGTATCATAC ATCCCAACAC GCATACATGT TTGCCTTCGA AGTATCTGGA

       1800          1810          1820          1830          1840          1850          1860
CGGTATTGAG ATTGCGATAT CGATGCAACC TGCGAATTGG CGATGTAATC AGTCATATTC TTACTAAACT
GCCATAACTC TAACGCTATA GCTACGTTGG ACGCTTAACC GCTACATTAG TCAGTATAAG AATGATTTGA

       1870          1880          1890          1900          1910          1920          1930
GCGAGACAGT GGTTTGTTTG CAATTGCAAT ATTTTTGTAT GGGGCTGCTT AAACTGTCAT TGCCTTTTTA
CGCTCTGTCA CCAAACAAAC GTTAACGTTA TAAAAACATA CCCCGACGAA TTTGACAGTA ACGGAAAAAT

       1940          1950          1960          1970          1980          1990          2000
GATTGGCAAT ATGTGACTTT ATGCAAGTAT TTGATTGGGC GGATCCAGGA ACAAAAAGTT GGGGGGATTC
CTAACCGTTA TACACTGAAA TACGTTCATA AACTAACCCG CCTAGGTCCT TGTTTTTCAA CCCCCCTAAG

       2010          2020          2030          2040          2050          2060          2070
AACATACCGA GTACACTGGC ATAAACACAT CATCTCAGTA TTAAACTATG CTAAAATGCT ATTAAGAGAC
TTGTATGGCT CATGTGACCG TATTTGTGTA GTAGAGTCAT AATTTGATAC GATTTTACGA TAATTCTCTG
```

Fig. 2C

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      2080        2090        2100        2110        2120        2130        2140
CTTTAGCACC TCTTATCTTA TCAACCATGG TGAAAAAATT GAAGGGGGGA CTCAGGGGGG TATCCATGGG
GAAATCGTGG AGAATAGAAT AGTTGGTACC ACTTTTTTAA CTTCCCCCCT GAGTCCCCCC ATAGGTACCC

      2150        2160        2170        2180        2190        2200        2210
TCCGATGGGT GCAGGGGGGA CTGAGTCCCC CCTGCACCCA CGTTGAATCC GCCCTGGCAT GCGTATAAGC
AGGCTACCCA CGTCCCCCCT GACTCAGGGG GGACGTGGGT GCAACTTAGG CGGGACCGTA CGCATATTCG

      2220        2230        2240        2250        2260        2270        2280
TGTCACAGCC ATTTCTAGGT GCTTGTGCTT AGTTGGGTGA TGTCAGCTTA ATTTGTCTTT TCTATGTCGT
ACAGTGTCGG TAAAGATCCA CGAACACGAA TCAACCCACT ACAGTCGAAT TAAACAGAAA AGATACAGCA

      2290        2300        2310        2320        2330        2340        2350
CATCGATTTT CTAAGAAACG AAAAATAGCC TATTTATGTG CTCCAGAATT TGATGATCCC TGGCCCTTCA
GTAGCTAAAA GATTCTTTGC TTTTTATCGG ATAAATACAC GAGGTCTTAA ACTACTAGGG ACCGGGAAGT

      2360        2370        2380        2390        2400        2410        2420
TTTGCTGAAA TTAGCCTATT TGTTGGTTGC CCTTCAGTTT TTTCCCAGCT TATGTTGTTG CAATGTGTGG
AAACGACTTT AATCGGATAA ACAACCAACG GGAAGTCAAA AAAGGGTCGA ATACAACAAC GTTACACACC

      2430        2440        2450        2460        2470        2480        2490
CTATGCCTCG TTTTGTGCCC TATAATTTAT TATTTGCAAT TCATTTTTGT ACATGACTTA AAATGACACT
GATACGGAGC AAAACACGGG ATATTAAATA ATAAACGTTA AGTAAAAACA TGTACTGAAT TTTACTGTGA

      2500        2510        2520        2530        2540        2550        2560
AGAGCAACAT GCACTGATTG GTTATCCTAT AATCATTTAT GTAGTTCTGT TCATTTTATC ATGCTAGCTC
TCTCGTTGTA CGTGACTAAC CAATAGGATA TTAGTAAATA CATCAAGACA AGTAAAATAG TACGATCGAG

      2570        2580        2590        2600        2610        2620
ATGTCATTTT CATCTTCAG GCC TCT GGC ACA GTT CCA CCT GAG CGT CCT GGA GCT GGT TCA
TACAGTAAAA GTAGAAGTC CGG AGA CCG TGT CAA GGT GGA CTC GCA GGA CCT CGA CCA AGT
                        A   S   G   T   V   P   P   E   R   P   G   A   G   S>
                   ___b___b___b___b___b____EXON2__b___b___b___b___b___b___b___>

      2630        2640        2650        2660        2670        2680
TCC TTG CTG AAT GCA GAT GTT TCA CAC ATA GGC GCT CCT AAT TCC ATC GGA GGTACTTA
AGG AAC GAC TTA CGT CTA CAA AGT GTG TAT CCG CGA GGA TTA AGG TAG CCT CCATGAAT
 S   L   L   N   A   D   V   S   H   I   G   A   P   N   S   I   G>
___b___b___b___b___b___b___b__EXON2____b___b___b___b___b___b___b___>

      2690        2700        2710        2720        2730        2740        2750
TCTTATCTGG TTACATTTTC AGATTGTTAT GAAACTACCC AAATATCCTG CACAATTGCA TGGGATTAAA
AGAATAGACC AATGTAAAAG TCTAACAATA CTTTGATGGG TTTATAGGAC GTGTTAACGT ACCCTAATTT
```

Fig. 2D

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      2760       2770       2780       2790       2800       2810       2820
TTTTAGTTTC TTTGAAATAG AAGTAGAGTT GTATTGCTGT CACGTCATCA AATAGTTCTG AAGCTATGAA
AAAATCAAAG AAACTTTATC TTCATCTCAA CATAACGACA GTGCAGTAGT TTATCAAGAC TTCGATACTT

      2830       2840       2850       2860       2870       2880       2890
TAAATAAGTT CCGCATTTGT TAGTGATTCT TTGAACATTA GAATTGTTAT GCTTAAGTAG ATAGGGTTAT
ATTTATTCAA GGCGTAAACA ATCACTAAGA AACTTGTAAT CTTAACAATA CGAATTCATC TATCCCAATA

      2900       2910       2920       2930       2940       2950       2960
GTTTGTTTGG AGTTCCCTTA AATCATTTCA TTGCTGACTG CCAGCTGGCA GGAGCATTTG TTGTTGCCTT
CAAACAAACC TCAAGGGAAT TTAGTAAAGT AACGACTGAC GGTCGACCGT CCTCGTAAAC AACAACGGAA

      2970       2980       2990       3000       3010       3020       3030
GACCATGAAT GAAGACCTTC CTGTTCTGAG TGCTCACAAG AAAACATATT TTGATTAATG CACCTTGAAT
CTGGTACTTA CTTCTGGAAG GACAAGACTC ACGAGTGTTC TTTTGTATAA AACTAATTAC GTGGAACTTA

      3040       3050       3060       3070       3080       3090       3100
CCTTAGGATC TTGCAAAGAT GGGCACTTAG CTTTAGAATT GAGTAGTACT TAAATAGCTG TTGTTATCAT
GGAATCCTAG AACGTTTCTA CCCGTGAATC GAAATCTTAA CTCATCATGA ATTTATCGAC AACAATAGTA

      3110       3120       3130       3140       3150       3160       3170
GATTTGTCCT GTAGTGAAAT GTCGACAAAA CAGGAATGCT ACTTTTGACT TCTGATATTT CATGCCTGGC
CTAAACAGGA CATCACTTTA CAGCTGTTTT GTCCTTACGA TGAAAACTGA AGACTATAAA GTACGGACCG

      3180       3190       3200        3210         3220          3230
TTTACTTATG CTCTGTTTGG AACATGGGCA CATATCA GGC AAT GCT ACT CCA GTT CAA AAC ATG
AAATGAATAC GAGACAAACC TTGTACCCGT GTATAGT CCG TTA CGA TGA GGT CAA GTT TTG TAC
                                          G   N   A   T   P   V   Q   N   M>
                                         ____c____c____c__EXON3 ____c____c____c____>


   3240        3250        3260        3270         3280        3290
CTA AGT GGC CCA AGT GGG GGA TCG GGC TCA CAG TTG GTA CAG AAT GTT GAT GTC CTT
GAT TCA CCG GGT TCA CCC CCT AGC CCG AGT GTC AAC CAT GTC TTA CAA CTA CAG GAA
 L   S   G   P   S   G   G   S   G   S   Q   L   V   Q   N   V   D   V   L>
____c____c____c____c____c____c____c____c__EXON3 ____c____c____c____c____c____c____c____c____>

      3300        3310        3320        3330        3340
GTA AAG CAG CCC ACC AGC TCT TCA TCA AGG GAG CAG TCA GAT GAT GAT GAC ATG AAG
CAT TTC GTC GGG TGG TCG AGA AGT AGT TCC CTC GTC AGT CTA CTA CTA CTG TAC TTC
 V   K   Q   P   T   S   S   S   S   R   E   Q   S   D   D   D   D   M   K>
____c____c____c____c____c____c____c____c__EXON3 ____c____c____c____c____c____c____c____c____>

3350       3360        3370        3380        3390        3400
GGA GAA GCT GAG ACC ACT GGA ACT GCA AGA CCT GCT GAT CAA AGA TTA CAA CGA
CCT CTT CGA CTC TGG TGA CCT TGA CGT TCT GGA CGA CTA GTT TCT AAT GTT GCT
 G   E   A   E   T   T   G   T   A   R   P   A   D   Q   R   L   Q   R>
____c____c____c____c____c____c____c_____EXON3 _c____c____c____c____c____c____c____c____>
```

Fig. 2E

```
    3410        3420        3430        3440        3450        3460        3470
AGGTGATC ATTCATTGCT TCCTTGTAAT ATAGATTCTG TACATAATTA ACCTACCTCG TCATGCATGC
TCCACTAG TAAGTAACGA AGGAACATTA TATCTAAGAC ATGTATTAAT TGGATGGAGC AGTACGTACG

    3480        3490        3500        3510        3520        3530        3540
ATGTGTCCTA TTTTCACCTT AGCCCTTTCA GTTGGATTTC CACTTTCATC CGGTAGCCTT TCAGTTTCCT
TACACAGGAT AAAAGTGGAA TCGGGAAAGT CAACCTAAAG GTGAAAGTAG GCCATCGGAA AGTCAAAGGA

    3550        3560        3570        3580        3590        3600        3610
ATTGCATCGC ATATATGATC TTTTACCTAC CATATTAGTT CTCTGTGTGC CATACTCAGT GCTTAGTGTC
TAACGTAGCG TATATACTAG AAAATGGATG GTATAATCAA GAGACACACG GTATGAGTCA CGAATCACAG

    3620        3630        3640        3650        3660        3670        3680
TCGAGCAAGA GAGGAATTTG TATGGCTATT ACACGTAGCA CTTTGCTCTC TACTTGTTTA TTGACATAAG
AGCTCGTTCT CTCCTTAAAC ATACCGATAA TGTGCATCGT GAAACGAGAG ATGAACAAAT AACTGTATTC

    3690        3700        3710        3720        3730        3740        3750
CAATTTGGGA TGAATTAAAT CTGAGTTCAC ATCATATTCC TTATGTCACA AGTTTCTGAA ACCGATTGTA
GTTAAACCCT ACTTAATTTA GACTCAAGTG TAGTATAAGG AATACAGTGT TCAAAGACTT TGGCTAACAT

    3760        3770        3780        3790        3800        3810        3820
TCTAGTATCT GGTTGATGCA CCCCCATCTT GGATTTGCAA ATCAAAGTTA TACTCCCTAG AGAGCTTTAC
AGATCATAGA CCAACTACGT GGGGGTAGAA CCTAAACGTT TAGTTTCAAT ATGAGGGATC TCTCGAAATG

    3830        3840        3850        3860        3870        3880        3890
CTTTCATAAA GCAATTACCC CAATAAACCA CGGATTTGAT AGCTATTGAC TATGATTACC AGAATTCATT
GAAAGTATTT CGTTAATGGG GTTATTTGGT GCCTAAACTA TCGATAACTG ATACTAATGG TCTTAAGTAA

    3900        3910        3920        3930        3940        3950        3960
TGGCAGCTAT TTTCTCAATT TAAGTTTGGT ATTAGTCTCA GTTGGCTGTA AAATAATGTC ACGGTAGGGT
ACCGTCGATA AAAGAGTTAA ATTCAAACCA TAATCAGAGT CAACCGACAT TTTATTACAG TGCCATCCCA

    3970        3980        3990        4000        4010        4020        4030
ACATGTATGT GCAGCATACA AGGTATGGGT GAGTTATGAT ATGGACAGTG TGTACACCCC ACATTTGCTC
TGTACATACA CGTCGTATGT TCCATACCCA CTCAATACTA TACCTGTCAC ACATGTGGGG TGTAAACGAG

    4040        4050        4060        4070        4080        4090        4100
ACTAAAATCA AAATATTCAA ACGTCACGTG ATGATATGGT GGATTGCATT ATACCTTGTA TTGTTTATTA
TGATTTTAGT TTTATAAGTT TGCAGTGCAC TACTATACCA CCTAACGTAA TATGGAACAT AACAAATAAT

    4110        4120        4130        4140        4150        4160        4170
TGTTACTTGT GCTAGACAAT AATATAGGCT GTTCTTTTGG GTGATTTTGT ATGAAGATGT TGAGCAAGCA
ACAATGAACA CGATCTGTTA TTATATCCGA CAAGAAAACC CACTAAAACA TACTTCTACA ACTCGTTCGT

    4180        4190        4200        4210        4220        4230
CTTCTCGATA TAATGCTAGT TTTGTTGACC TGTTCC AGG AAG CAA TCC AAT CGG GAG TCA GCC
GAAGAGCTAT ATTACGATCA AAACAACTGG ACAAGG TCC TTC GTT AGG TTA GCC CTC AGT CGG
                                      R   K   Q   S   N   R   E   S   A>
                                    ___d___d___d__EXON4____d___d___d___d___>
```

Fig. 2F

4240 4250 4260 4270 4280 4290
AGG CGC TCA AGA AGC AGA AAG GCA GCT CAC TTG AAT GAG CTG GAG GCA CAG GTGTGA
TCC GCG AGT TCT TCG TCT TTC CGT CGA GTG AAC TTA CTC GAC CTC CGT GTC CACACT
R R S R S R K A A H L N E L E A Q>
___d___d___d___d___d___d___d__EXON4_____d___d___d___d___d___d___d___>

4300 4310 4320 4330 4340 4350 4360
TAGTTCACAT AGTTATTTTC GATAAGACAT AAAATCCTAA ATTACTGGCT ACTGACTTCA GTTATGGATT
ATCAAGTGTA TCAATAAAAG CTATTCTGTA TTTTAGGATT TAATGACCGA TGACTGAAGT CAATACCTAA

4370 4380 4390 4400 4410 4420
TACTTGTTAC AG GTA TCG CAA TTA AGA GTC GAG AAC TCC TCG CTG TTA AGG CGT CTT GCT
ATGAACAATG TC CAT AGC GTT AAT TCT CAG CTC TTG AGG AGC GAC AAT TCC GCA GAA CGA
V S Q L R V E N S S L L R R L A>
____e___e___e___e___e___e_____EXON5__e___e___e___e___e___e___e___>

4430 4440 4450 4460 4470
GAT GTT AAC CAG AAG TAC AAT GAT GCT GCT GTT GAC AAT AGA GTG CTA AAA GCA GAT
CTA CAA TTG GTC TTC ATG TTA CTA CGA CGA CAA CTG TTA TCT CAC GAT TTT CGT CTA
D V N Q K Y N D A A V D N R V L K A D>
____e___e___e___e___e___e___e___e__EXON5_____e___e___e___e___e___e___e___e___>

4480 4490 4500 4510 4520 4530 4540
GTT GAG ACC TTG AGA GCA AAG GT ATGCTATATA TGCCTTTTGC AATATGCATC CCATGGATTG
CAA CTC TGG AAC TCT CGT TTC CA TACGATATAT ACGGAAAACG TTATACGTAG GGTACCTAAC
V E T L R A K>
____e___e__EXON5_____e___e___>

4550 4560 4570 4580 4590 4600 4610
CTACTTTGGC TTGTTTCAAA CTTTCAACGT GACTTGTGTA CCCTGTTATT AGAAGAATAA TCCCGCCTAC
GATGAAACCG AACAAAGTTT GAAAGTTGCA CTGAACACAT GGGACAATAA TCTTCTTATT AGGGCGGATG

4620 4630 4640 4650 4660 4670 4680
CATTATACTC TATAAATCAC CATTTGGCCA GTCCAAACAT GATTATTAAA TCAGGTCAAT CTGAACATTG
GTAATATGAG ATATTTAGTG GTAAACCGGT CAGGTTTGTA CTAATAATTT AGTCCAGTTA GACTTGTAAC

4690 4700 4710 4720 4730 4740
AAATGTATCA AAAATTCGCA GGTG AAG ATG GCA GAG GAC TCG GTG AAG CGG GTG ACA GGC
TTTACATAGT TTTTAAGCGT CCAC TTC TAC CGT CTC CTG AGC CAC TTC GCC CAC TGT CCG
K M A E D S V K R V T G>
___f___f___f___f_____EXON6__f___f___f___f___f___>

4750 4760 4770 4780 4790
ATG AAC GCG TTG TTT CCC GCC GCT TCT GAT ATG TCA TCC CTC AGC ATG CCA TTC AAC
TAC TTG CGC AAC AAA GGG CGG CGA AGA CTA TAC AGT AGG GAG TCG TAC GGT AAG TTG
M N A L F P A A S D M S S L S M P F N>
____f___f___f___f___f___f___f___f__EXON6_____f___f___f___f___f___f___f___f___>

Fig. 2G

```
4800          4810          4820          4830          4840          4850
AGC TCC CCA TCT GAA GCA ACG TCA GAC GCT GCT GTT CCC ATC CAA GAT GAC CCG AAC
TCG AGG GGT AGA CTT CGT TGC AGT CTG CGA CGA CAA GGG TAG GTT CTA CTG GGC TTG
 S   S   P   S   E   A   T   S   D   A   A   V   P   I   Q   D   D   P   N>
___f___f___f___f___f___f___f___f__EXON6____f___f___f___f___f___f___f___f___>

   4860          4870          4880          4890          4900          4910
AAT TAC TTC GCT ACT AAC AAC GAC ATC GGA GGT AAC AAC AAC TAC ATG CCC GAC ATA
TTA ATG AAG CGA TGA TTG TTG CTG TAG CCT CCA TTG TTG TTG ATG TAC GGG CTG TAT
 N   Y   F   A   T   N   N   D   I   G   G   N   N   N   Y   M   P   D   I>
___f___f___f___f___f___f___f___f__EXON6____f___f___f___f___f___f___f___f___>

         4920          4930          4940          4950          4960
CCT TCT TCG GCT CAG GAG GAC GAG GAC TTC GTC AAT GGC GCT CTG GCT GCC GGC AAG
GGA AGA AGC CGA GTC CTC CTG CTC CTG AAG CAG TTA CCG CGA GAC CGA CGG CCG TTC
 P   S   S   A   Q   E   D   E   D   F   V   N   G   A   L   A   A   G   K>
___f___f___f___f___f___f___f___f__EXON6____f___f___f___f___f___f___f___f___>

         4970          4980          4990          5000          5010
5020
ATT GGC CGG CCA GCC TCG CTG CAG CGG GTG GCG AGC CTG GAG CAT CTC CAG AAG AGG
TAA CCG GCC GGT CGG AGC GAC GTC GCC CAC CGC TCG GAC CTC GTA GAG GTC TTC TCC
 I   G   R   P   A   S   L   Q   R   V   A   S   L   E   H   L   Q   K   R>
___f___f___f___f___f___f___f___f__EXON6____f___f___f___f___f___f___f___f___>

   5030          5040          5050          5060          5070          5080
ATG TGC GGT GGG CCG GCT TCG TCT GGG TCG ACG TCC TGA GACCGA AACCCAGAGC
TAC ACG CCA CCC GGC CGA AGC AGA CCC AGC TGC AGG ACT CTGGCT TTGGGTCTCG
 M   C   G   G   P   A   S   S   G   S   T   S   *>
___f___f___f___f___f__EXON6____f___f___f___f___f___>

         5090          5100          5110          5120          5130          5140          5150
TGCTTCGGTT CTGAAAGACA CTGCGAGCAG GAAATGATGA TTGGACAGGC GTAGACATTG CTAATGCTGT
ACGAAGCCAA GACTTTCTGT GACGCTCGTC CTTTACTACT AACCTGTCCG CATCTGTAAC GATTACGACA

         5160          5170          5180          5190          5200          5210          5220
GAGGTTGATG ATTGTTGGTC GTCGTCGTCG TCATTGTGCA TTCTTTGTAA GGGACACCTC TTAGTACCCT
CTCCAACTAC TAACAACCAG CAGCAGCAGC AGTAACACGT AAGAAACATT CCCTGTGGAG AATCATGGGA

         5230          5240          5250          5260          5270          5280          5290
CTTCTTCTAA GGGACTTAGT ACCCCTTGTG GATCTCATCG TCCTAAATAC TATACACATT AGCCAAATGT
GAAGAAGATT CCCTGAATCA TGGGGAACAC CTAGAGTAGC AGGATTTATG ATATGTGTAA TCGGTTTACA

>terminator                                                                  |
         5300          5310          5320          5330          5340          5350          5360
TCATTGGTGT GATGGCGTCG TCCCTAATTT GAACGACTGA TTTCAGGCAG CTGCTATGCT ATCATTCAAT
AGTAACCACA CTACCGCAGC AGGGATTAAA CTTGCTGACT AAAGTCCGTC GACGATACGA TAGTAAGTTA
```

Fig. 2H

```
      5370        5380        5390        5400        5410        5420        5430
AATATTTTGA TCGATGCTTC CTCTTGTCTT TTGCTCTTAA GCAACCAAGC ATAAAGATAT CACTACCTTT
TTATAAAACT AGCTACGAAG GAGAACAGAA AACGAGAATT CGTTGGTTCG TATTTCTATA GTGATGGAAA

      5440        5450        5460        5470        5480        5490        5500
TGAGCTGTTC ATTTGAAGTG CAAAGCTAAG CTCAATATCT CAGGTGTTCA TTTGAAGTTT AAAGGTGAAC
ACTCGACAAG TAAACTTCAC GTTTCGATTC GAGTTATAGA GTCCACAAGT AAACTTCAAA TTTCCACTTG

      5510        5520        5530        5540        5550        5560        5570
TGATAACAAA CGTCAGGCTA TGGTGAATGA AGGGACGTGT ACATCCCTAA TACATGTCAT TTTCATAATC
ACTATTGTTT GCAGTCCGAT ACCACTTACT TCCCTGCACA TGTAGGGATT ATGTACAGTA AAAGTATTAG

      5580        5590        5600        5610        5620        5630        5640
AAATTAGTTG ATGCATTTTC ACCCAGAATC CCATCACAGT TCATCATACA AGCAAGTGTA GTTATTAATG
TTTAATCAAC TACGTAAAAG TGGGTCTTAG GGTAGTGTCA AGTAGTATGT TCGTTCACAT CAATAATTAC

      5650        5660        5670        5680        5690        5700        5710
GTAAATTTTT CGTTTAGAGA AAAAAAAAGG AAGCCTTATA TAAGATTCAC CGGTGGGGTG TGAACAATAA
CATTTAAAAA GCAAATCTCT TTTTTTTTCC TTCGGAATAT ATTCTAAGTG GCCACCCCAC ACTTGTTATT

      5720        5730        5740        5750        5760        5770        5780
TCAATGAATG AGATCGCATC CCGTAAGGGC AGCCTAGCTA GACAAAAATG CATAAAACTC CGTATACCAA
AGTTACTTAC TCTAGCGTAG GGCATTCCCG TCGGATCGAT CTGTTTTTAC GTATTTTGAG GCATATGGTT

      5790        5800        5810        5820        5830        5840        5850
CCACAACAAC GCTTGCGCAC GCGCTCAAAT GGCAGCGACT TCATCGCTTT CGCGGGCAAG AAACGAATCA
GGTGTTGTTG CGAACGCGTG CGCGAGTTTA CCGTCGCTGA AGTAGCGAAA GCGCCCGTTC TTTGCTTAGT

      5860        5870        5880        5890        5900        5910        5920
AGTGATACAT TGGCAGGGAA CCACCAAAAG AAGGCCATCC AATCCAATCC ACTCCAACGC GGCATGGAAG
TCACTATGTA ACCGTCCCTT GGTGGTTTTC TTCCGGTAGG TTAGGTTAGG TGAGGTTGCG CCGTACCTTC

      5930        5940        5950        5960        5970        5980        5990
ACAAGACAGA TGATTCACAG CTATCTTCTG CTTCTACAAG TTTGATACTT TGTACTGTCC TTTCAGGGAA
TGTTCTGTCT ACTAAGTGTC GATAGAAGAC GAAGATGTTC AAACTATGAA ACATGACAGG AAAGTCCCTT

      6000        6010        6020        6030        6040        6050        6060
AAAAGAGCAT CAGATTAGTC TGATCTCGGG CGCGTTGAGT TCTTGTGGGA GATCTTGTTG TGGAGTGGCA
TTTTCTCGTA GTCTAATCAG ACTAGAGCCC GCGCAACTCA AGAACACCCT CTAGAACAAC ACCTCACCGT

      6070        6080        6090        6100        6110        6120        6130
GGAGTGACGA TCGGCTGCCC CGTTTTCTTC TACCGAAACA TCGCCAGTAA AGAAGCCAAA AAGACAATAA
CCTCACTGCT AGCCGACGGG GCAAAAGAAG ATGGCTTTGT AGCGGTCATT TCTTCGGTTT TTCTGTTATT

      6140        6150        6160        6170        6180        6190        6200
TACGGCAATG GGGATCGCCC ATCTGCATAA AACATTGCAT GACGGAACTG ATTAATACAA GAATGACATG
ATGCCGTTAC CCCTAGCGGG TAGACGTATT TTGTAACGTA CTGCCTTGAC TAATTATGTT CTTACTGTAC

      6210        6220
TAAGCTGATA ATTACGCGTG CAAGCTT
ATTCGACTAT TAATGCGCAC GTTCGAA
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Fig. 2I

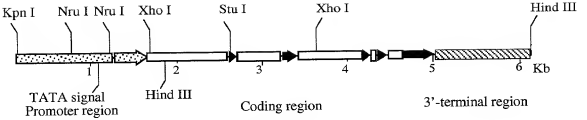
Kpn I
Nru I
Nru I
Xho I
Stu I
Xho I
Hind III
1
2
3
4
5
6
Kb
TATA signal
Promoter region
Hind III
Coding region
3'-terminal region

Fig. 3

```
        10         20         30         40         50         60         70         80         90
AAGCTTGCAT GCCTGCAGGG AGGAGAGGGG AGAGATGGTG AGAGAGGAGG AAGAAGAGGA GGGGTGACAA TGATATGTGG GCCATGTGGC
                                                                  >Reb_site1
                                                                                       |
       100        110        120        130        140        150        160        170        180
CCCCACCATT TTTTAATTCA TTCTTTTGTT GAAACTGACA TGTGGGTCCC ATGAGAATTA TTATTTTTCG GATCGAATT GCCACGTAAGC

                                        >Reb_site1   >reb_site2
                                        |            |
       190        200        210        220        230        240        250        260        270
GCTACGTCAA TGCTACGTCA GATGAAGACC GAGTCAAATT AGCCACGTAAG CGCCACGTCAG CCAAAACC ACCATCCAAA CCGCCGAGGG

       280        290        300        310        320        330        340        350        360
ACCTCATCTG CACTGGTTTT GATAGTTGAG GGACCCGTTG TATCTGGTTT TTCGATTGAA GGACGAAAAT CAAATTTGTT GACAAGTTAA

       370        380        390        400        410        420        430        440        450
GGGACCTTAA ATGAACTTAT TCCATTTCAA AATATTCTGT GAGCCATATA TCCGTGGGCT TCCAATCCTC CTCAAATTAA AGGGCCTTTT

       460        470        480        490        500        510        520        530        540
TAAAATAGAT AATTGCCTTC TTTCAGTCAC CCATAAAAGT ACAAAACTAC TACCAACAAG CAACATGCGC AGTTACACAC ATTTTCTGCA

       550        560        570        580        590        600        610        620        630
CATTTCCACC ACGTCACAAA GAGCTAAGAG TTATCCCTAG GACAATCTCA TTAGTGTAGA TACATCCATT AATCTTTTAT CAGAGGCAAA

       640        650        660        670        680        690        700        710        720
CGTAAAGCCG CTCTTTATGA CAAAAATAGG TGACACAAAA GTGTTATCTG CCACATACAT AACTTCAGAA ATTACCCAAC ACCAAGAGAA

       730        740        750        760        770        780        790        800        810
AAATAAAAAA AAATCTTTTT GCAAGCTCCA AATCTTGGAA ACCTTTTTCA CTCTTTGCAG CATTGTACTC TTGCTCTTTT TCCAACCGAT

       820        830        840        850        860        870        880        890        900
CCATGTCACC CTCAAGCTTC TACTTGATCT ACACGAAGCT CACCGTGCAC ACAACCATGG CCACAAAAAC CCTATAAAAC CCCATCCGAT

       910        920        930        940        950        960        970        980        990
CGCCATCATC TCATCATCAG TTCATCACCA ACAAACAAAA GAGGAAAAAA AACATATACA CTTCTAGTGA TTGTCTGATT GATCATCAAT

      1000       1010       1020       1030       1040       1050       1060
CTAGAGGATC CCCGGGTGGT CAGTCCCTT ATG
                          Gus Start site
```

Fig. 4

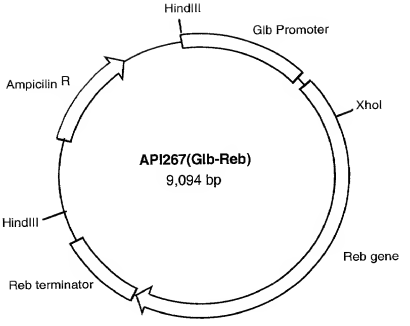
HindIII
Glb Promoter
Ampicilin R
XhoI
API267(Glb-Reb)
9,094 bp
HindIII
Reb gene
Reb terminator

Fig. 5A

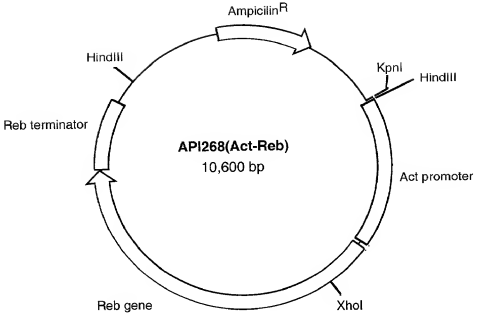
Ampicilin^R
HindIII
KpnI
HindIII
Reb terminator
API268(Act-Reb)
10,600 bp
Act promoter
Reb gene
XhoI

Fig. 5B

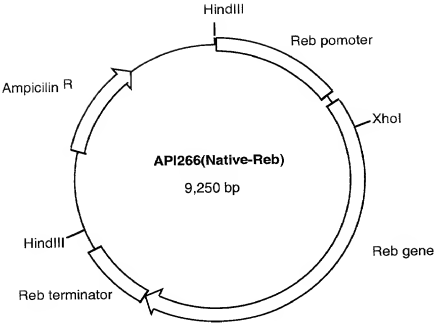
HindIII
Reb pomoter
Ampicilin R
XhoI
API266(Native-Reb)
9,250 bp
HindIII
Reb gene
Reb terminator

Fig. 5C

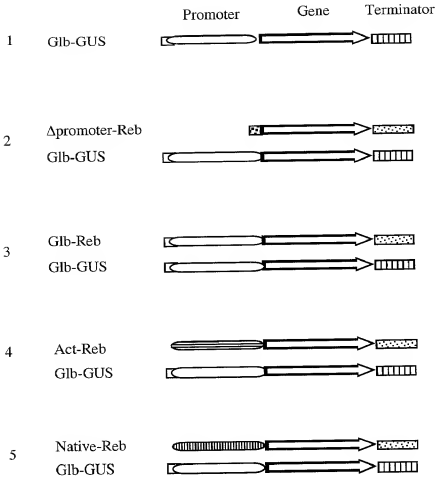
Promoter
Gene
Terminator
1
Glb-GUS
2
Δpromoter-Reb
Glb-GUS
3
Glb-Reb
Glb-GUS
4
Act-Reb
Glb-GUS
5
Native-Reb
Glb-GUS

Fig. 6A

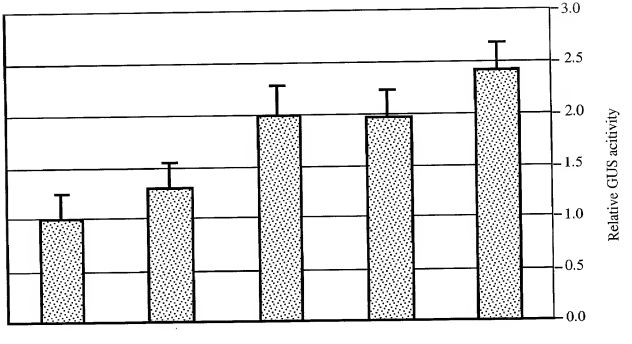
3.0
2.5
2.0
1.5
1.0
0.5
0.0
Relative GUS acitivity

Fig. 6B

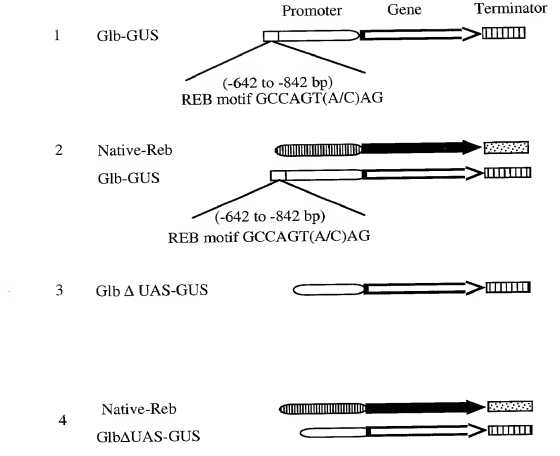
Promoter
Gene
Terminator
1
Glb-GUS
(-642 to -842 bp)
REB motif GCCAGT(A/C)AG
2
Native-Reb
Glb-GUS
(-642 to -842 bp)
REB motif GCCAGT(A/C)AG
3
Glb Δ UAS-GUS
4
Native-Reb
GlbΔUAS-GUS

Fig. 7A

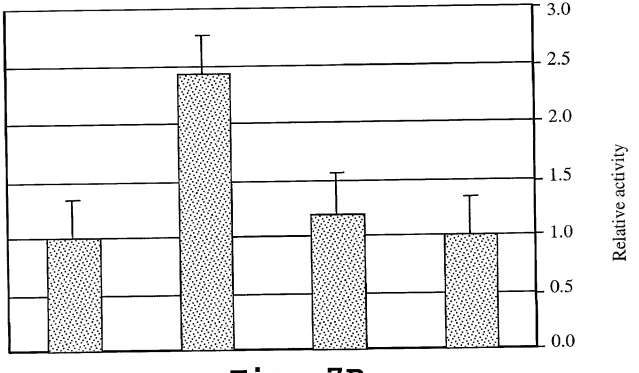
3.0
2.5
2.0
1.5
1.0
0.5
0.0
Relative activity

Fig. 7B

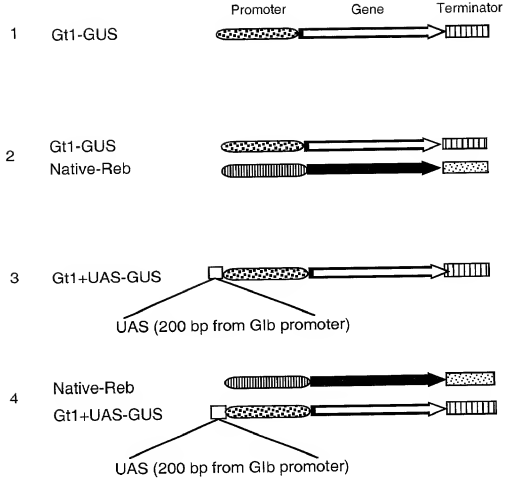
Promoter
Gene
Terminator
1
Gt1-GUS
2
Gt1-GUS
Native-Reb
3
Gt1+UAS-GUS
UAS (200 bp from Glb promoter)
4
Native-Reb
Gt1+UAS-GUS
UAS (200 bp from Glb promoter)

Fig. 8A

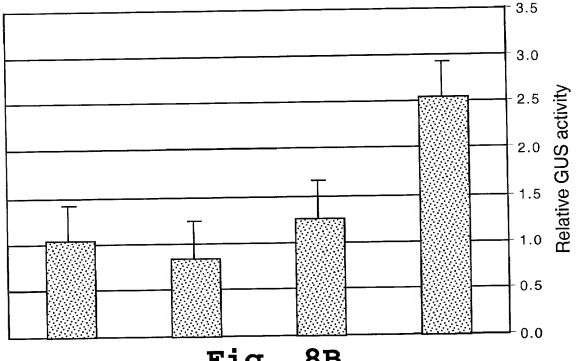
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
Relative GUS activity

Fig. 8B

```
10        20        30        40        50        60        70        80        90        100
CTGCAGGGAGGAGAGGGGAGAGATGGTGAGAGAGGAGGAAGAAGAGGAGGGGTGACAATGATATGTGGGCCATGTGGCCCCCACCATTTTTTAATTCATT

                                                  ACGT core  ACGT core  ACGT core
110       120       130       140       150       160|      170|      180|      190       200
CTTTTGTTGAAACTGACATGTGGGTCCCATGAGAATTATTATTTTTCGGATCGAATTGCCACGTAAGCGCTACGTCAATGCTACGTCAGATGAAGACCGA

ACGT core  ACGT core
210 |      220|      230       240       250       260       270       280       290       300
GTCAAATTAGCCACGTAAGCGCCACGTCAGCCAAAACCACCATCCAAACCGCCGAGGGACCTCATCTGCACTGGTTTTGATAGTTGAGGGACCCGTTGTA

310       320       330       340       350       360       370       380       390       400
TCTGGTTTTTCGATTGAAGGACGAAAATCAAATTTGTTGACAAGTTAAGGGACCTTAAATGAACTTATTCCATTTCAAAATATTCTGTGAGCCATATATC

410       420       430       440       450       460       470       480       490       500
CGTGGGCTTCCAATCCTCCTCAAATTAAAGGGCCTTTTTAAAATAGATAATTGCCTTCTTTCAGTCACCCATAAAAGTACAAAACTACTACCAACAAGCA

                              ACGT core
510       520       530       540       550       560       570       580       590       600
ACATGCGCAGTTACACACATTTTCTGCACATTTCCACCACGTCACAAAGAGCTAAGAGTTATCCCTAGGACAATCTCATTAGTGTAGATACATCCATTAA

        ACGT core
        |prolaminbox
        ||
610     620       630       640       650       660       670       680       690       700
TCTTTTATCAGAGGCAAACGTAAAGCCGCTCTTTATGACAAAAATAGGTGACACAAAAGTGTTATCTGCCACATACATAACTTCAGAAATTACCCAACAC

                                                        prolaminbox
                                                        |
710       720       730       740       750       760   770       780       790       800
CAAGAGAAAAATAAAAAAAAATCTTTTTGCAAGCTCCAAATCTTGGAAACCTTTTTCACTCTTTGCAGCATTGTACTCTTGCTCTTTTTCCAACCGATCC

                                                            TATA_box
810       820       830       840       850       860       870|      880       890       900
ATGTCACCCTCAAGCTTCTACTTGATCTACACGAAGCTCACCGTGCACACAACCATGGCCACAAAAACCCTATAAAACCCCATCCGATCGCCATCATCTC

txn_start_site
|
910       920       930       940       950       960       970       980
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Fig. 9

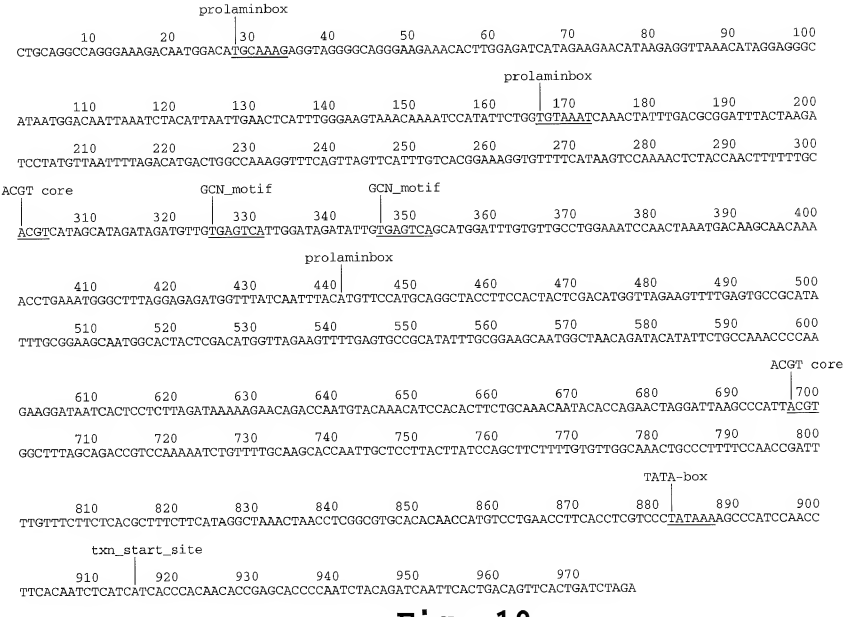
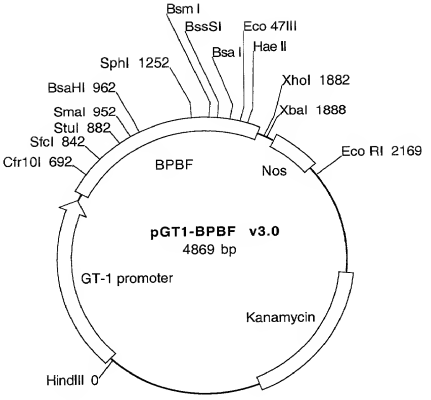

prolaminbox
prolaminbox
ACGT core
GCN_motif
GCN_motif
prolaminbox
ACGT core
TATA-box
txn_start_site

Fig. 10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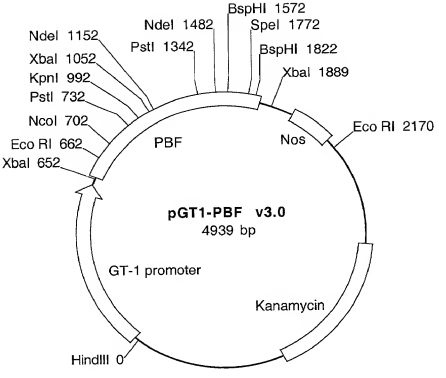
BssSI
Eco 47III
Hae II
Bsa I
SphI 1252
XhoI 1882
BsaHI 962
SmaI 952
XbaI 1888
StuI 882
SfcI 842
Cfr10I 692
BPBF
Nos
Eco RI 2169
pGT1-BPBF v3.0
4869 bp
GT-1 promoter
Kanamycin
HindIII 0

Fig. 11A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NdeI 1482
SpeI 1772
NdeI 1152
PstI 1342
BspHI 1822
XbaI 1052
XbaI 1889
KpnI 992
PstI 732
NcoI 702
PBF
Nos
EcoRI 2170
EcoRI 662
XbaI 652
pGT1-PBF v3.0
4939 bp
GT-1 promoter
Kanamycin
HindIII 0

Fig. 11B

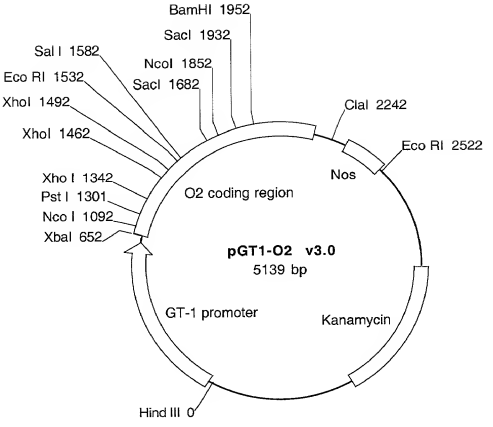
BamHI 1952
SacI 1932
Sal I 1582
NcoI 1852
Eco RI 1532
SacI 1682
XhoI 1492
ClaI 2242
XhoI 1462
Eco RI 2522
Nos
Xho I 1342
O2 coding region
Pst I 1301
Nco I 1092
XbaI 652
pGT1-O2 v3.0
5139 bp
GT-1 promoter
Kanamycin
Hind III 0

Fig. 11C

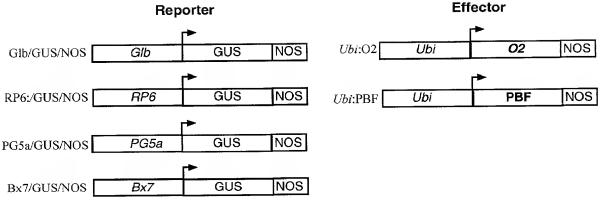

Fig. 12A

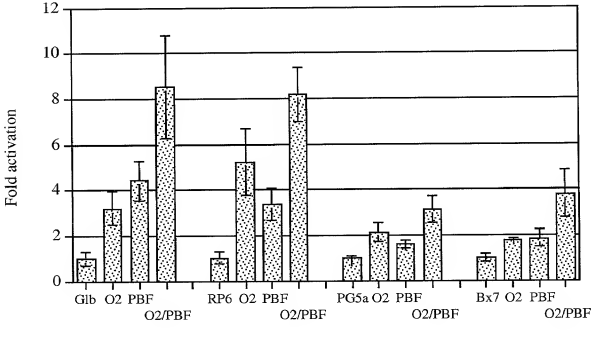

Fig. 12B

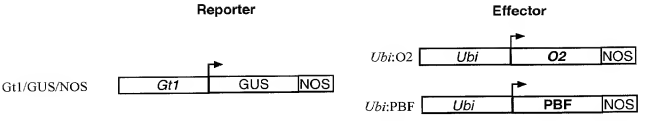

Fig. 13A

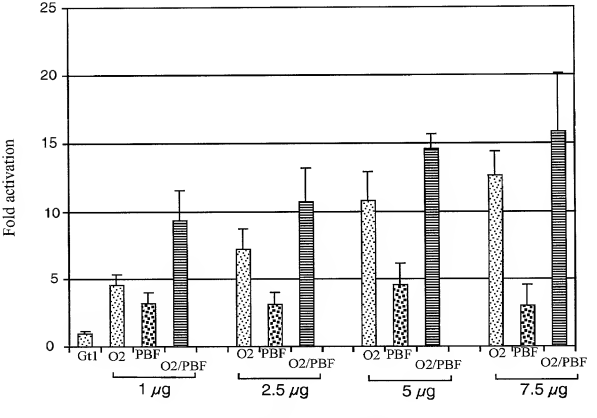

Fig. 13B

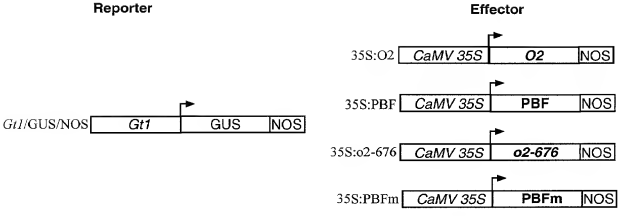

Fig. 14A

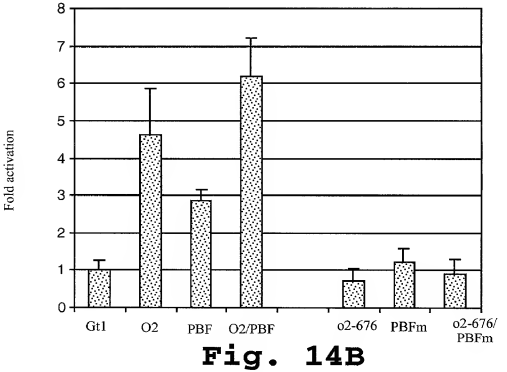

Fig. 14B

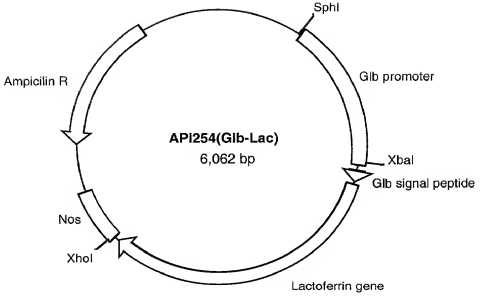
SphI
Glb promoter
Ampicilin R
API254(Glb-Lac)
6,062 bp
XbaI
Glb signal peptide
Nos
XhoI
Lactoferrin gene

Fig. 15A

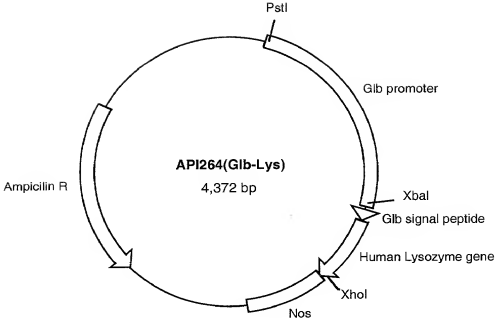
PstI
Glb promoter
API264(Glb-Lys)
4,372 bp
Ampicilin R
XbaI
Glb signal peptide
Human Lysozyme gene
XhoI
Nos

Fig. 15B

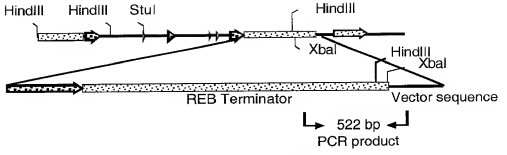

Fig. 16A

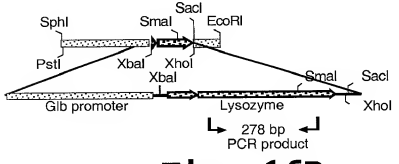

Fig. 16B

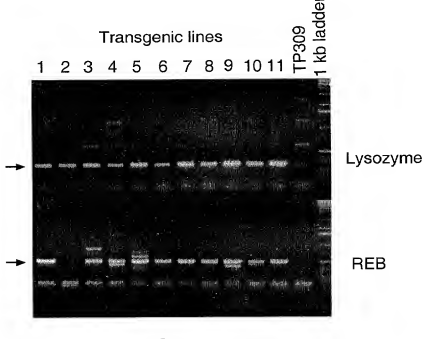

Fig. 16C

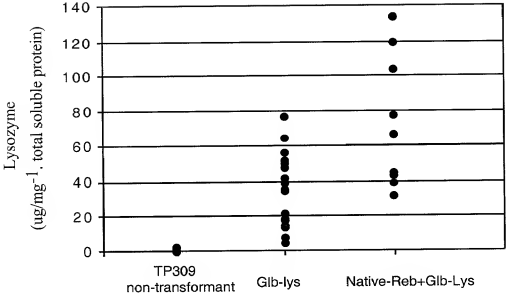
Lysozyme
(ug/mg-1. total soluble protein)
140
120
100
80
60
40
20
0
TP309
non-transformant
Glb-lys
Native-Reb+Glb-Lys

Fig. 17